



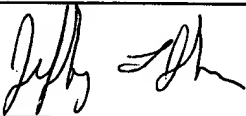
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE	<i>Application Number</i>	09/550,163
	<i>Filing Date</i>	April 14, 2000
	<i>First Named Inventor</i>	Geoffrey W. ABBOTT et al.
	<i>Group Art Unit</i>	1655
	<i>Examiner Name</i>	Brian Whiteman
	<i>Attorney Docket Number</i>	2323-150
<i>Title of the Invention:</i> MINK-RELATED GENES, FORMATION OF POTASSIUM CHANNELS AND ASSOCIATION WITH CARDIAC ARRHYTHMIA		

Response to Raw Sequence Listing Error Report

Director of the United States
Patent and Trademark Office
P.O. Box 1450
Alexandria, Virginia 22313-1540

Sir:

In response to the Notice of Raw sequence Listing Error Report (copy attached), Applicants hereby submit the attached Substitute Sequence Listing. Also submitted herewith is a computer readable form with a copy of the Substitute Sequence Listing and a statement that the copy in computer readable form is the same as the substitute copy of the Sequence Listing.

RESPECTFULLY SUBMITTED,			
<i>NAME AND REG. NUMBER</i>	Jeffrey L. Ihnen, Reg. No. 28,957		
<i>SIGNATURE</i>		<i>DATE</i>	15 July 2004

<i>Address</i>	ROTHWELL, FIGG, ERNST & MANBECK, pc 1425 K Street, N.W., Suite 800				
<i>City</i>	Washington	<i>State</i>	D.C.	<i>Zip Code</i>	20005
<i>Country</i>	U.S.A.	<i>Telephone</i>	202-783-6040	<i>Fax</i>	202-783-6031



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/550,163B
 Source: FW/b
 Date Processed by STIC: 11/29/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/efc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
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Revised 10/08/03

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Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/550,1638
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	

AMC - Biotechnology Systems Branch - 09/09/2003

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IFW16

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/550,163B

DATE: 12/29/2003
 TIME: 18:29:45

Input Set : A:\09550163b.txt
 Output Set: N:\CRF4\12292003\I550163B.raw

3 <110> APPLICANT: University of Utah Research Foundation
 4 Yale University
 5 Abbott, Geoffrey W
 6 Sesti, Federico
 7 Splawski, Igor
 8 Keating, Mark T
 9 Goldstein, Steve A.N.
 11 <120> TITLE OF INVENTION: Mink-Related Genes, Formation of Potassium Channels and
 12 Association with Cardiac Arrhythmia
 14 <130> FILE REFERENCE: 2323-150.a
 16 <140> CURRENT APPLICATION NUMBER: 09/550,163B
 17 <141> CURRENT FILING DATE: 2000-04-14
 19 <150> PRIOR APPLICATION NUMBER: US 60/129,404
 20 <151> PRIOR FILING DATE: 1999-04-15
 22 <160> NUMBER OF SEQ ID NOS: 22
 23 <170> SOFTWARE: PatentIn version 3.1/2.0

Does Not Comply
 Corrected Diketone Needed
 pp 1-3

ERRORED SEQUENCES

774 <210> SEQ ID NO: 21
 775 <211> LENGTH: 130
 776 <212> TYPE: PRT
 777 <213> ORGANISM: rattus norvegicus
 E--> 779 <400> SEQUENCE: 321
 781 Met Ala Leu Ser Asn Ser Thr Thr Val Leu Pro Phe Leu Ala Ser Leu
 782 1 5 10 15
 785 Trp Gln Glu Thr Asp Glu Pro Gly Gly Asn Met Ser Ala Asp Leu Ala
 786 20 25 30
 789 Arg Arg Ser Gln Leu Arg Asp Asp Ser Lys Leu Glu Ala Leu Tyr Ile
 790 35 40 45
 793 Leu Met Val Leu Gly Phe Phe Gly Phe Phe Thr Leu Gly Ile Met Leu
 794 50 55 60
 797 Ser Tyr Ile Arg Ser Lys Lys Leu Glu His Ser His Asp Pro Phe Asn
 798 65 70 75 80
 801 Val Tyr Ile Glu Ser Asp Ala Trp Gln Glu Lys Gly Lys Ala Leu Phe
 802 85 90 95
 805 Gln Ala Arg Val Leu Glu Ser Phe Arg Ala Cys Tyr Val Ile Glu Asn
 806 100 105 110
 809 Gln Ala Ala Val Glu Gln Pro Ala Thr His Leu Pro Glu Leu Lys Pro
 810 115 120 125
 813 Leu Ser
 814 130

RAW SEQUENCE LISTING

DATE: 12/29/2003

PATENT APPLICATION: US/09/550,163B

TIME: 18:29:45

Input Set : A:\09\550163b.txt

Output Set: N:\CRF4\12292003\I550163B.raw

817 <210> SEQ ID NO: 22
818 <211> LENGTH: 129
819 <212> TYPE: PRT
820 <213> ORGANISM: homo sapiens
E--> 823 <400> SEQUENCE: 022
825 Met Ile Leu Ser Asn Thr Thr Ala Val Thr Pro Phe Leu Thr Lys Leu
826 1 5 10 15
829 Trp Gln Glu Thr Val Gln Gln Gly Gly Asn Met Ser Gly Leu Ala Arg
830 20 25 30
833 Arg Ser Pro Arg Ser Gly Asp Gly Lys Leu Glu Ala Leu Tyr Val Leu
834 35 40 45
837 Met Val Leu Gly Phe Phe Gly Phe Phe Thr Leu Gly Ile Met Leu Ser
838 50 55 60
841 Tyr Ile Arg Ser Lys Lys Leu Glu His Ser Asn Asp Pro Phe Asn Val
842 65 70 75 80
845 Tyr Ile Glu Ser Asp Ala Trp Gln Glu Lys Asp Lys Ala Tyr Val Gln
846 85 90 95
849 Ala Arg Val Leu Glu Ser Tyr Arg Ser Cys Tyr Val Val Glu Asn His
850 100 105 110
853 Leu Ala Ile Glu Gln Pro Asn Thr His Leu Pro Glu Thr Lys Pro Ser
854 115 120 125
857 Pro

see p. 3

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3

<210> 19
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HA residues for
epitope mapping

<220>

<221> PEPTIDE

<222> (10)

<223> Xaa represents encoded stop codon.

<400> 19

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Xaa
1 5 10

Xaa cannot represent a stop
codon,

Since a
stop codon
cannot
encode an
amino acid
(see item 13 on
Error summary
sheet)

same error in sequence 20

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VERIFICATION SUMMARY

DATE: 12/29/2003

PATENT APPLICATION: US/09/550,163B

TIME: 18:29:46

Input Set : A:\09550163b.txt

Output Set: N:\CRF4\12292003\I550163B.raw

L:751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0

L:769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0

L:779 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:21 differs:3

L:823 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:22 differs:4